WHAT IS CLAIMED IS:

- 1. A method of quantitating the amount of a protein or peptide in a sample comprising:
 - (a) obtaining a sample containing said protein or peptide;
 - (b) providing a standard protein or peptide wherein the standard is a derivative of the protein or peptide of interest at a known or measurable quantity;
 - (c) co-crystallizing the protein or peptide and standard with a matrix;
 - (d) analyzing the crystallized target protein or peptide and standard using matrixassisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and
 - (e) determining the amount of the protein or peptide present in the sample based on the analysis in (d).
- 2. The method of claim 1, wherein said sample is derived from a cell.
- 3. The method of claim 2, wherein said cell is a prokaryotic cell.
- 4. The method of claim 2, wherein said cell is a eukaryotic cell.
- 5. The method of claim 2, wherein said cell is a mammalian cell.
- 6. The method of claim 2, wherein said cell is a human cell.
- 7. The method of claim 6, wherein said human cell is a cardiomyocte.
- 8. The method of claim 1, wherein said sample is derived from an organ.
- 9. The method of claim 8, wherein said organ is a heart.
- 10. The method of claim 8, wherein said sample is organ is a human heart.
- 11. The method of claim 1, wherein said sample is obtained from plasma.
- 12. The method of claim 1, wherein said sample is obtained from serum.

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- 13. The method of claim 1, wherein said source has been exposed to an agent that alters the expression or structure of the protein or peptide.
- 14. The method of claim 1, wherein the protein is alpha myosin heavy chain.
- 15. The method of claim 1, wherein the protein is beta myosin heavy chain.
- 16. The method of claim 1, wherein the protein is cardiac actin.
- 17. The method of claim 1, wherein the protein is skeletal actin.
- 18. The method of claim 1, wherein the peptide is produced by proteolytic cleavage.
- 19. The method of claim 1, wherein the peptide is produced by chemical cleavage.
- 20. The method of claim 1, wherein the peptide is produced by enzymatic digestion.
- 21. The method of claim 20, wherein the enzymatic digestion is performed by an endopeptidase.
- 22. The method of claim 20, wherein the enzymatic digestion is performed by a protease.
- 23. The method of claim 1, wherein the protein, peptide and/or standard are produced synthetically.
- 24. The method of claim 1, wherein the standard is designed by modifying a single amino acid from the target protein or peptide.
- 25. A method of quantitatively comparing the amount of a plurality of structurally distinct proteins or peptides in a sample comprising:
 - (a) obtaining one or more samples containing said multiply distinct target proteins or peptides;
 - (b) providing a standard protein or peptide for each target protein, wherein the standard is a derivative of the target protein or peptide of interest at a known or measurable quantity;
 - (c) co-crystallizing the target proteins or peptides and standard with a matrix;

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- (d) analyzing the crystallized target proteins or peptides and standard using matrixassisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and
- (e) determining relative or absolute amounts of each target protein or peptide analyzed that is present in the sample.
- 26. The method of claim 25, wherein the proteins are isoforms of each other.
- 27. The method of claim 26, wherein the isomers are phosphoisomers.
- 28. The method of claim 25, wherein said sample is derived from a cell.
- 29. The method of claim 28, wherein said cell is a prokaryotic cell.
- 30. The method of claim 28, wherein said cell is a eukaryotic cell.
- 31. The method of claim 28, wherein said cell is a mammalian cell.
- 32. The method of claim 28, wherein said cell is a human cell.
- 33. The method of claim 32, wherein said human cell is a cardiomyocte.
- 34. The method of claim 25, wherein said sample is derived from an organ.
- 35. The method of claim 34, wherein said sample organ is a heart.
- 36. The method of claim 34, wherein said organ is a human heart.
- 37. The method of claim 25, wherein said sample is obtained from plasma.
- 38. The method of claim 25, wherein said sample is obtained from serum.
- 39. The method of claim 25, wherein said source has been exposed to an agent that alters the expression or structure of the proteins or peptides.
- 40. The method of claim 25, wherein one of the proteins is α -myosin heavy chain.
- 41. The method of claim 25, wherein one of the proteins is β -myosin heavy chain.

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- 42. The method of claim 25, wherein one of the proteins is cardiac actin.
- 43. The method of claim 25, wherein one of the proteins is skeletal actin.
- 44. The method of claim 25, wherein the peptides are produced by proteolytic cleavage.
- 45. The method of claim 25, wherein the peptides are produced by chemical cleavage.
- 46. The method of claim 25, wherein the peptides are produced by enzymatic digestion.
- 47. The method of claim 46, wherein the enzymatic digestion is performed by an endopeptidase.
- 48. The method of claim 46, wherein the enzymatic digestion is performed by a protease.
- 49. The method of claim 25, wherein the proteins, peptides and/or standards are produced synthetically.
- 50. The method of claim 25, wherein the standards are proteins or peptides derived or synthesized directly from the proteins of interest.
- 51. The method of claim 25, wherein the standard are designed by modifying a single amino acid from the target proteins or peptides.
- 52. A method of determining relative amounts of at least two distinct proteins or peptides in a sample comprising:
 - (a) obtaining a samples containing said multiply distinct target proteins or peptides;
 - (b) co-crystallizing the target proteins or peptides and standard with a matrix;
 - (c) analyzing the crystallized target proteins or peptides using matrix- assisted laser dissorption/ionization time of flight (MALDI-TOF) mass spectrometry; and
 - (d) determining the relative amount of each target protein or peptide analyzed that is present in the sample.

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